Replacement Figure 1A
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

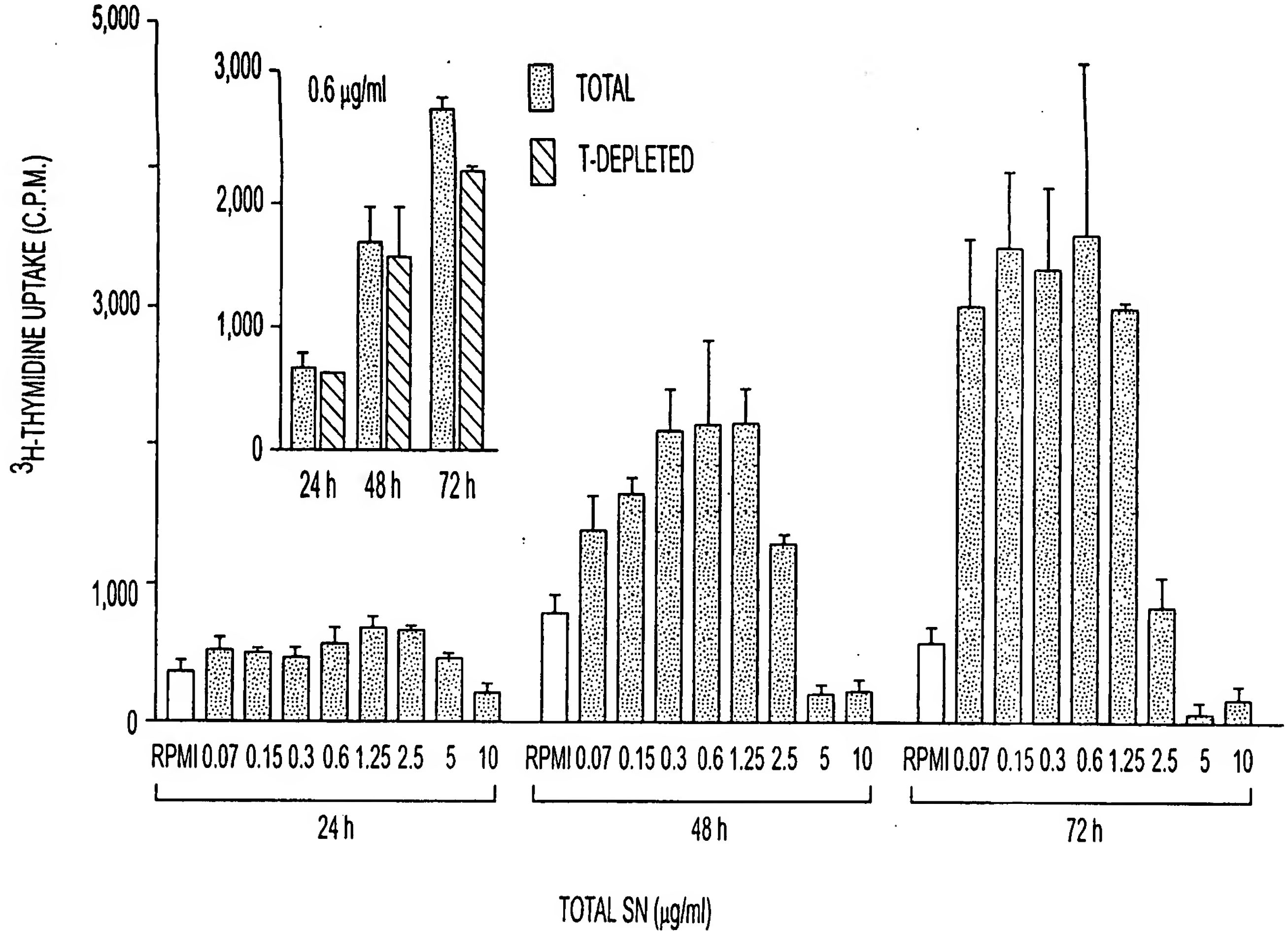


FIG. 1A

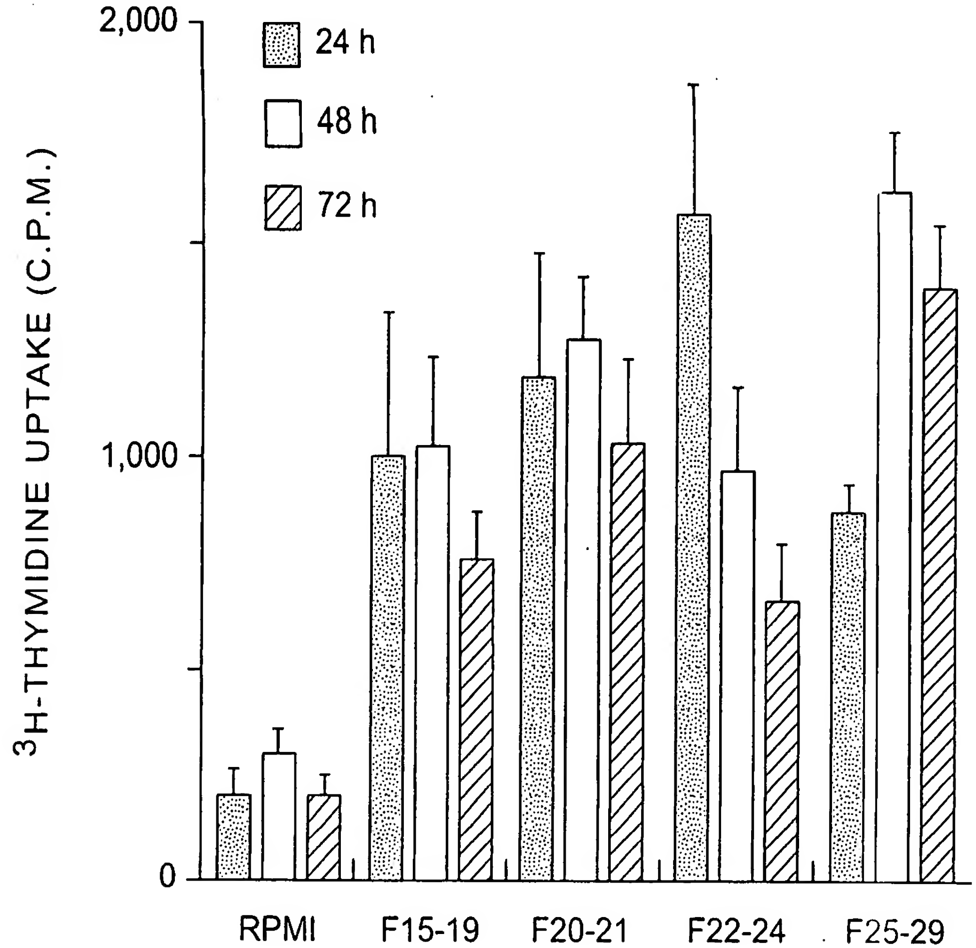

2,000
1,000
0
24 h
48 h
72 h
3H-THYMIDINE UPTAKE (C.P.M.)
RPMI
F15-19
F20-21
F22-24
F25-29

FIG. 1B

Replacement Figure 1C
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

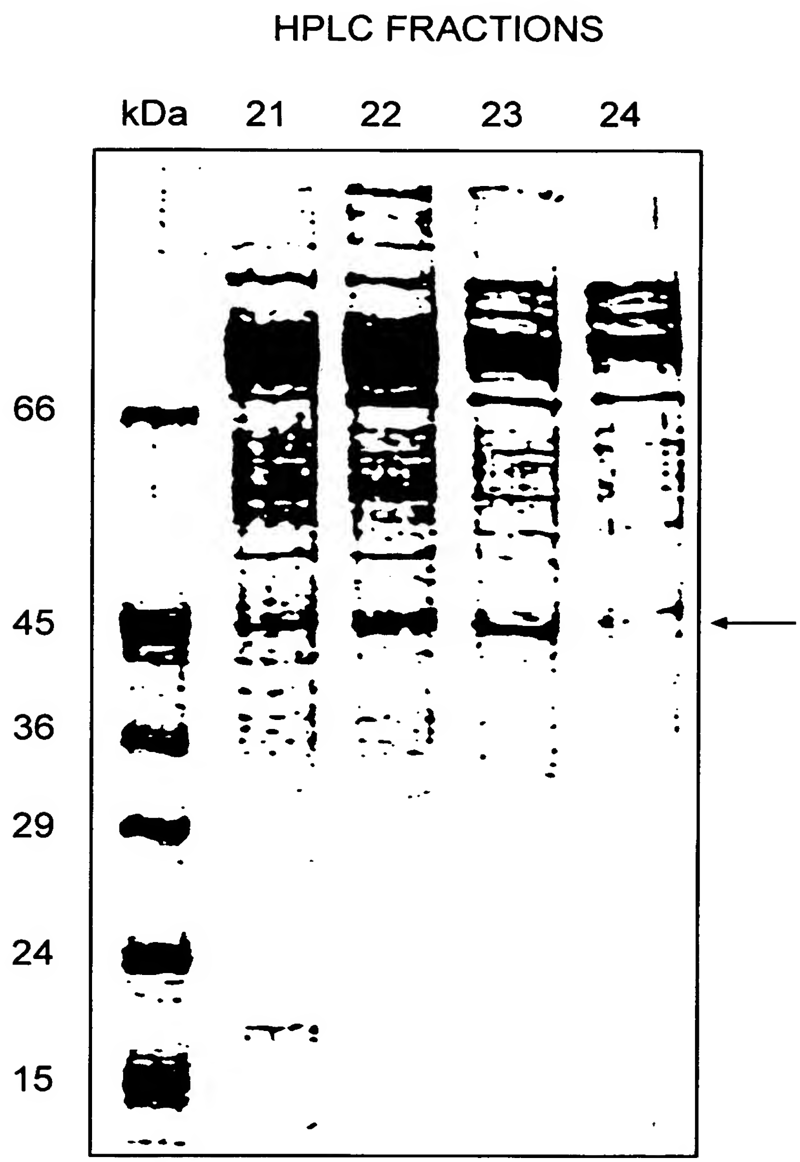


FIG. 1C

```
Tc  MRKSVCPKQKFFFSAFPFFFFFCVFPLISRTGQEKLLFDQKYKIIKGEKKEKKKNQRANRREHQQKREIMRFKKS   75
Cs  ---------------------------------------------------------------------MKFSKG    6
Pa  ------------------------------------------------------------------------MQR    3

Tc  FTCIDMHTEGEAARIVTSGLPHIPGSNMAEKKAYLQENMDYLRRGIMLEPRGHDDMFGAFLFDPIEEGADLGMVF  150
Cs  IHAIDSHTMGEPTRIVVGGIPQINGETMADKKKYLEDNLDYVRTALMHEPRGHNDMFGSIITSSNNKEADFGIIF   81
Pa  IRIIDSHTGGEPTRLVIGGFPDLGQGDMAERRRLLGERHDAWRAACILEPRGSDVLVGALLCAPVDPEACAGVIF   78

Tc  MDTGGYLNMCGHNSIAAVTAAVETGIVSVPAKATNVPVVLDTPAGLVRGTAHLQSGTESEVSNASIINVPSFLYQ  225
Cs  MDGGGYLNMCGHGSIGAATVAVETGMVEMVEPVTNIN--MEAPAGLIKAKVMVEN---EKVKEVSITNVPSFLYM  151
Pa  FNNSGYLGMCGHGTIGLVASLAHLGRIGPGV------HRIETPVGEVEATLH-------EDGSVSVRNVPAYRYR  140

Tc  QDVVVVLPKPYGEVRVDIAFGGNFFAIVPAEQLGIDISVQNLSRLQEAGELLRTEINRSVKVQHPQLPHINTVDC  300
Cs  EDAKLEVPSLNKTITFDISFGGSFFAIIHAKELGVKVETSQVDVLKKLGIEIRDLINEKIKVQHPELEHIKTVDL  226
Pa  RQVSVEVPGI-GRVSGDIAWGGNWFFLVAGH--GQRLAGDNLDALTAYTVAVQQALDD----QDIRGEDGGAIDH  208

Tc  VEIYGPPTNPEANYKNVVIFGNRQADR SPCGT GTSAKMATLYAKGQLRIGETFVYESILGSLFQGRV--LGEE  371
Cs  VEIYDEPSNPEATYKNVVIFGQGQVDR SPCGT GTSAKLATLYKKGHLKIDEKFVYESITGTMFKGRV--LEET  297
Pa  IELFAD--DPHADSRNFVLCPGKAYDR SPCGT GTSAKLACLAADGKLLPGQPWRQASVIGSQFEGRYEWLDGQ  279

Tc  RIPGVKVPVTKDAEEGMLVVTAEITGKAFIMGFNTMLFDPTDPFKNGFTLKQ*  423
Cs  KVGEFD------------AIIPEITGGAYITGFNHFVIDPEDPLKYGFTV*--  335
Pa  PGGPIVPTIRGRAHVSAEATLLLADDDPFAWGIRR*-----------------  314
```

FIG. 2

Replacement Figure 3A
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

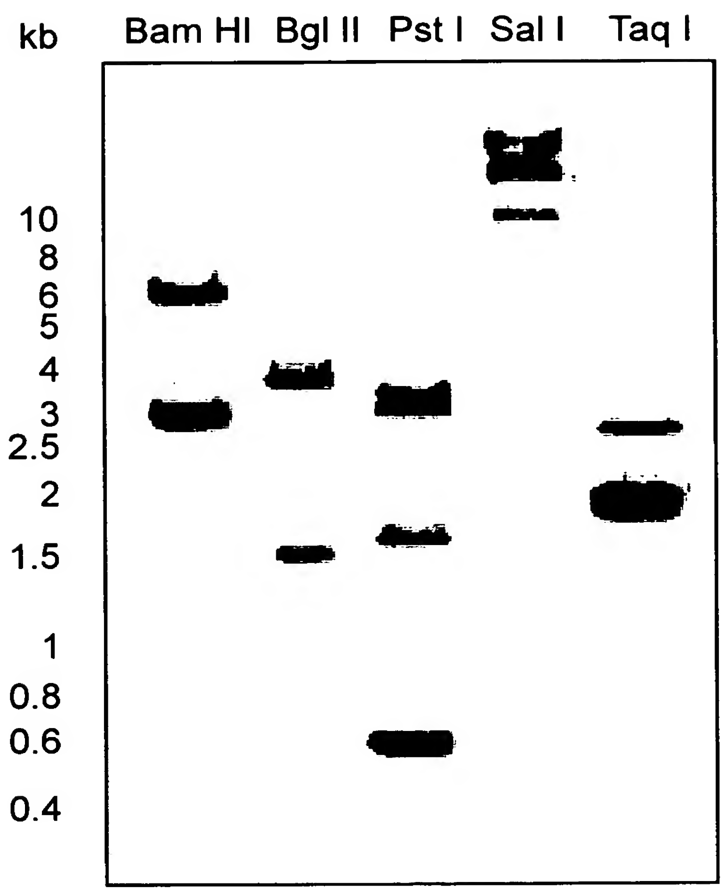


FIG. 3A

Replacement Figure 3B
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

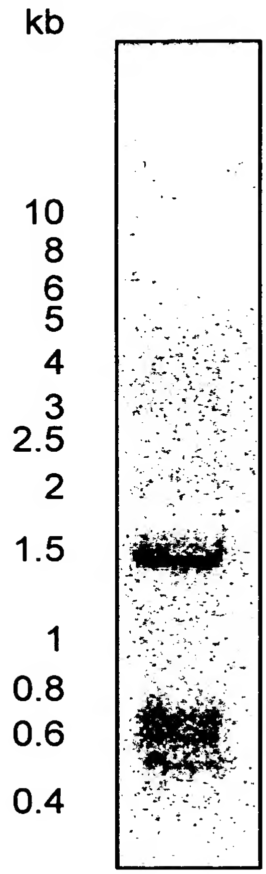


FIG. 3B

Replacement Figure 3C
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

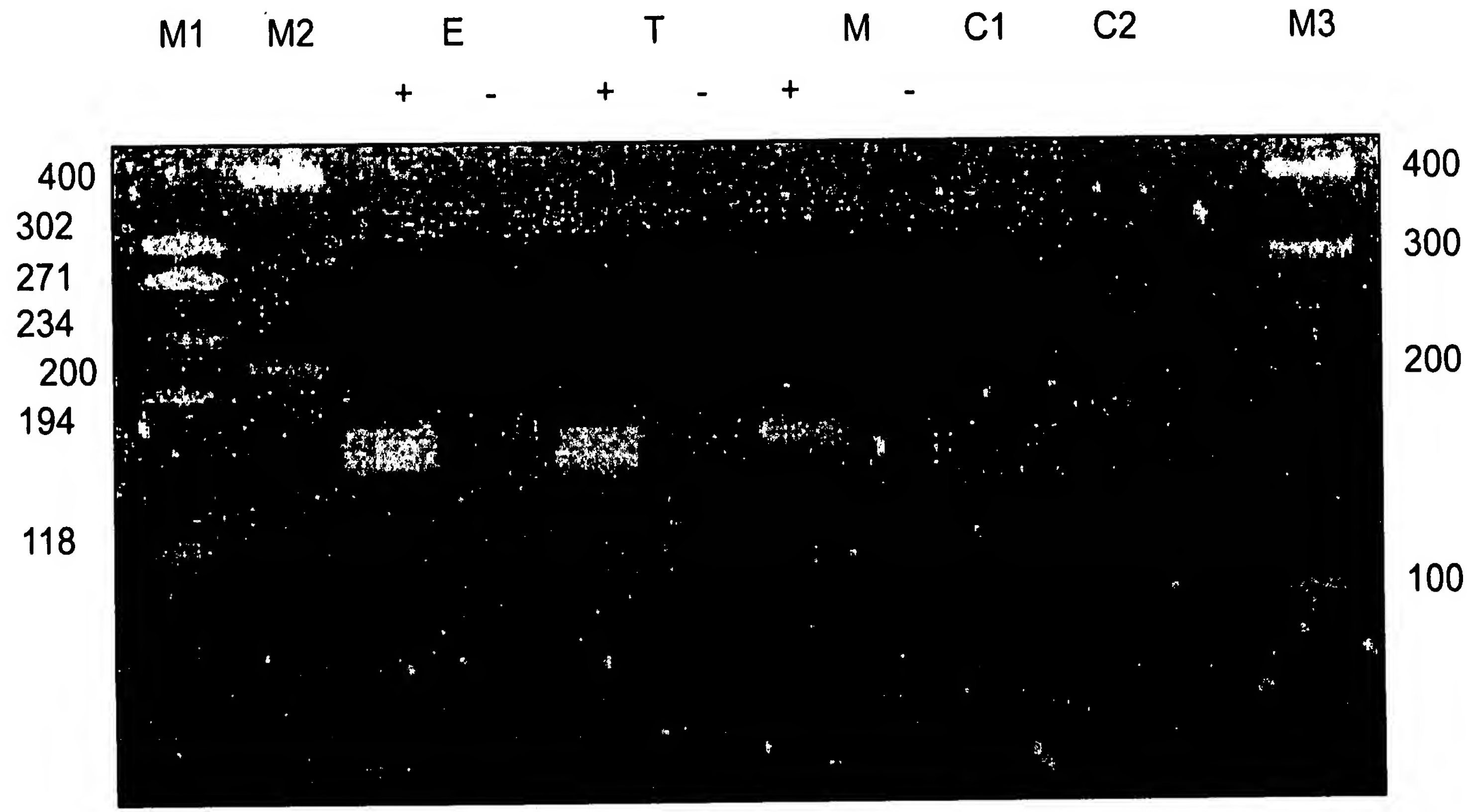


FIG. 3C

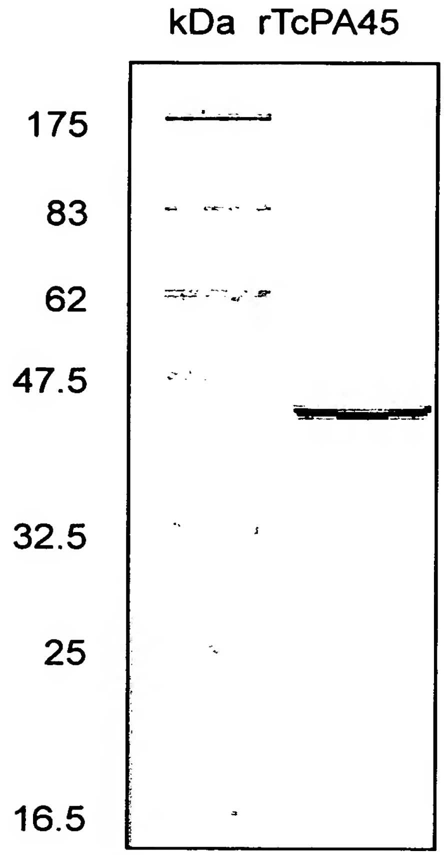


FIG. 4A

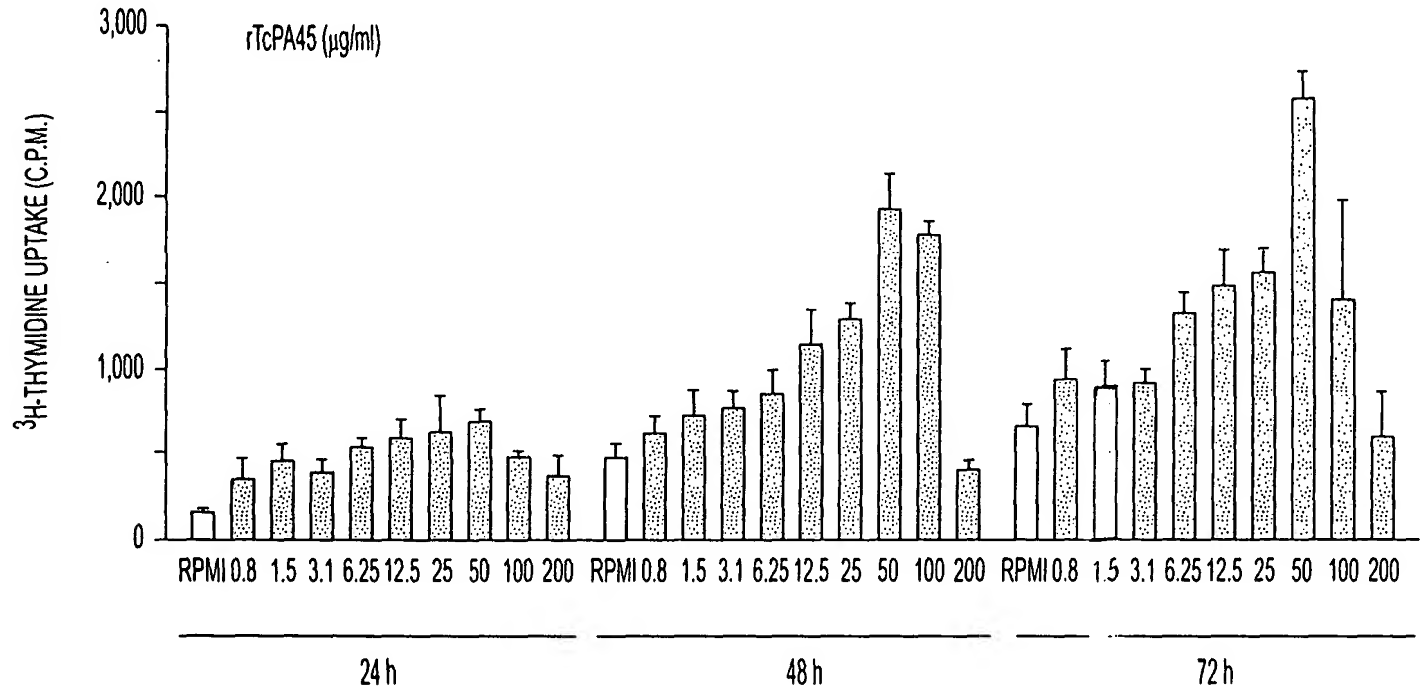

3,000
2,000
1,000
0
^{3}H-THYMIDINE UPTAKE (C.P.M.)
rTcPA45 (µg/ml)
RPMI 0.8 1.5 3.1 6.25 12.5 25 50 100 200
RPMI 0.8 1.5 3.1 6.25 12.5 25 50 100 200
RPMI 0.8 1.5 3.1 6.25 12.5 25 50 100 200
24 h
48 h
72 h

FIG. 4B

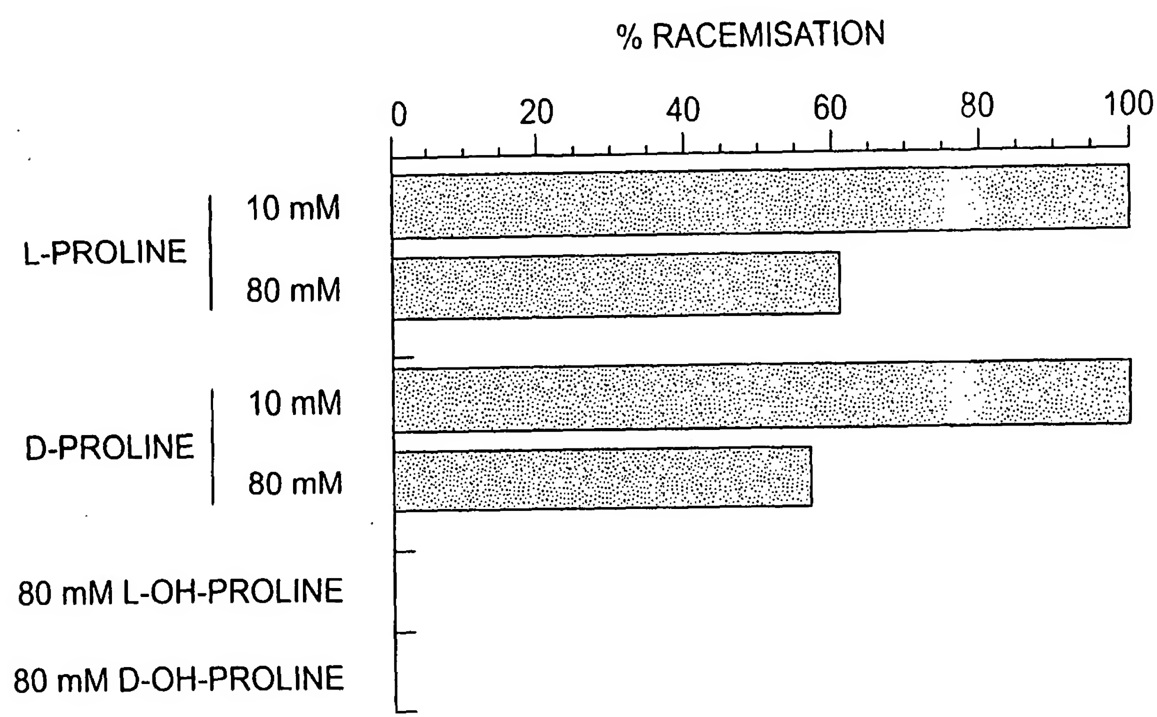

% RACEMISATION
0
20
40
60
80
100
L-PROLINE
10 mM
80 mM
D-PROLINE
10 mM
80 mM
80 mM L-OH-PROLINE
80 mM D-OH-PROLINE

FIG. 4C

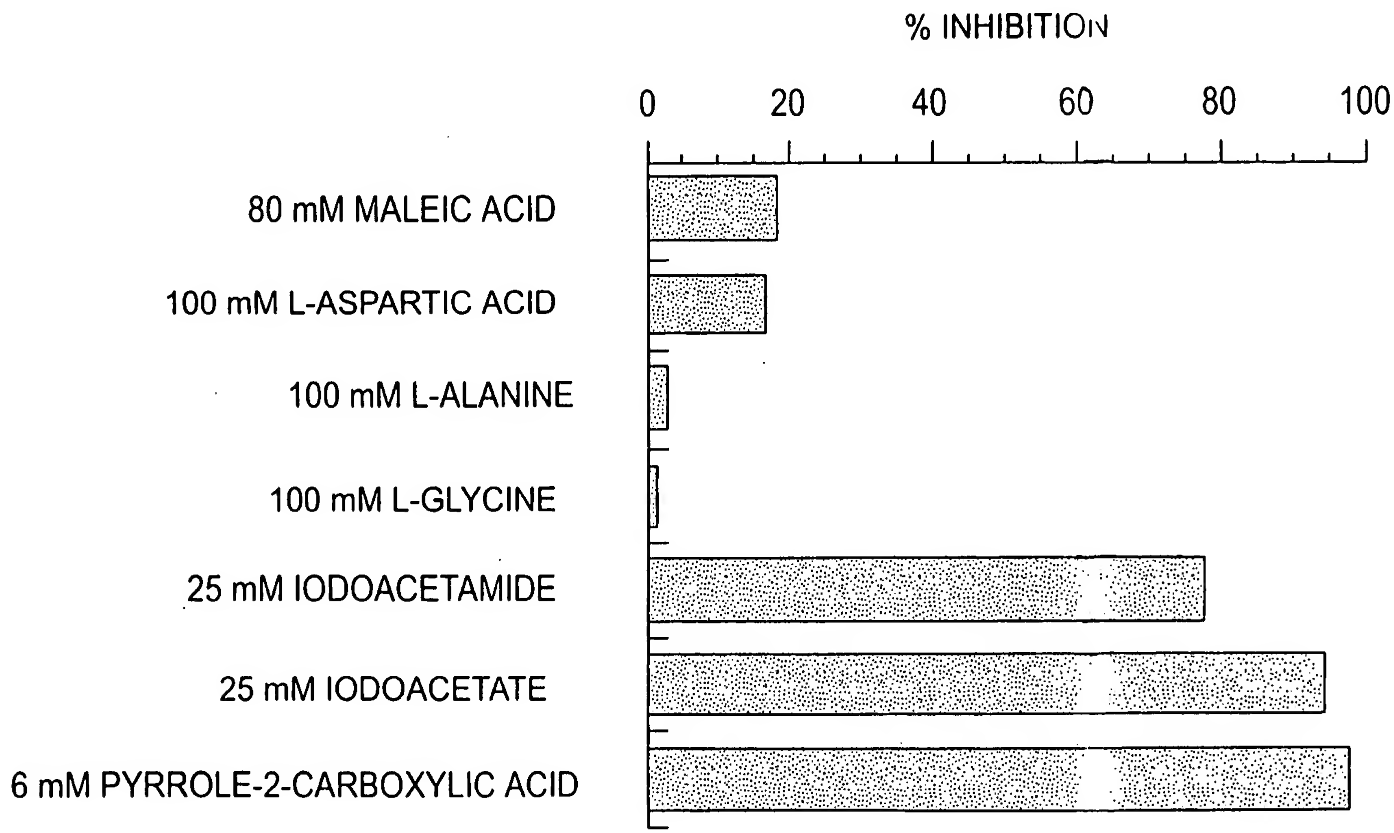

% INHIBITION
0
20
40
60
80
100
80 mM MALEIC ACID
100 mM L-ASPARTIC ACID
100 mM L-ALANINE
100 mM L-GLYCINE
25 mM IODOACETAMIDE
25 mM IODOACETATE
6 mM PYRROLE-2-CARBOXYLIC ACID

FIG. 4D

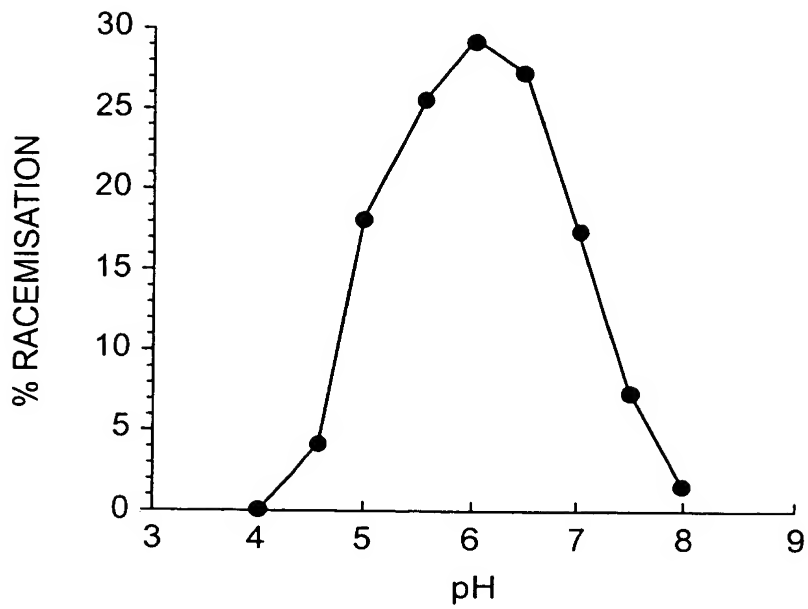


FIG. 4E

Replacement Figure 5A
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

POLYPYRIMIDINE RICH REGION

SPLICE LEADER ACCEPTOR SITES

SIGNAL

```
CCTTTTCTTTTTAAAAACAAAAAAAATTCCGGGGGGAATATGGAACAGGGTATATGCGTAAAAGTGTCTGTCCCAAACAAAAATTTTTT    90
                                                       M  R  K  S  V  C  P  K  Q  K  F  F    12
TTTTCCGCCTTCCCATTTTTTTTTTTTTTTGTGTGTTTCCCTTGATCTCTCGAACAGGGCAGGAAAAGCTTCTGTTTGACCAAAAATAT   180
 F  S  A  F  P  F  F  F  F  F  C  V  F  P  L  I  S  R  T  G  Q  E  K  L  L  F  D  Q  K  Y    42
AAAATTATTAAGGGCGAGAAAAAAGAAAAGAAAAAAAATCAACGAGCAAACAGGAGAGAACACCAACAAAAAAGGGAAATTATGCGATTT   270
 K  I  I  K  G  E  K  K  E  K  K  K  N  Q  R  A  N  R  R  E  H  Q  Q  K  R  E  I  M  R  F    72
AAGAAATCATTCACATGCATCGACATGCATACGGAAGGTGAAGCAGCACGGATTGTGACGAGTGGTTTGCCACACATTCCAGGTTCGAAT   360
 K  K  S  F  T  C  I  D  M  H  T  E  G  E  A  A  R  I  V  T  S  G  L  P  H  I  P  G  S  N   102
ATGGCGGAGAAGAAAGCATACCTGCAGGAAAACATGGATTATTTGAGGCGTGGCATAATGCTGGAACCACGTGGTCATGATGATATGTTT   430
 M  A  E  K  K  A  Y  L  Q  E  N  M  D  Y  L  R  R  G  I  M  L  E  P  R  G  H  D  D  M  F   132
GGAGCCTTTTTATTTGACCCTATTGAAGAAGGCGCTGACTTGGGCATGGTATTCATGGATACCGGTGGCTATTTAAATATGTGTGGACAT   520
 G  A  F  L  F  D  P  I  E  E  G  A  D  L  G  M  V  F  M  D  T  G  G  Y  L  N  M  C  G  H   162
AACTCAATTGCAGCGGTTACGGCGGCAGTTGAAACGGGAATTGTGAGCGTGCCGGCGAAGGCAACAAATGTTCCGGTTGTCCTGGACACA   610
 N  S  I  A  A  V  T  A  A  V  E  T  G  I  V  S  V  P  A  K  A  T  N  V  P  V  V  L  D  T   192
CCTGCGGGGTTGGTGCGCGGTACGGCACACCTTCAGAGTGGTACTGAGAGTGAGGTGTCAAATGCGAGTATTATCAATGTACCCTCATTT   700
 P  A  G  L  V  R  G  T  A  H  L  Q  S  G  T  E  S  E  V  S  N  A  S  I  I  N  V  P  S  F   222
TTGTATCAGCAGGATGTGGTGGTTGTGTTGCCAAAGCCCTATGGTGAAGTACGGGTTGATATTGCATTTGGAGGCAATTTTTTCGCCATT   790
 L  Y  Q  Q  D  V  V  V  V  L  P  K  P  Y  G  E  V  R  V  D  I  A  F  G  G  N  F  F  A  I   252
GTTCCCGCGGAGCAGTTGGGAATTGATATCTCCGTTCAAAACCTCTCCAGGCTGCAGGAGGCAGGAGAACTTCTGCGTACTGAAATCAAT   880
 V  P  A  E  Q  L  G  I  D  I  S  V  Q  N  L  S  R  L  Q  E  A  G  E  L  L  R  T  E  I  N   282
```

FIG. 5A

```
CGCAGTGTGAAGGTTCAGCACCCTCAGCTGCCCCATATTAACACTGTGGACTGTGTTGAGATATACGGTCCGCCAACGAACCCGGAGGCA   970
 R  S  V  K  V  Q  H  P  Q  L  P  H  I  N  T  V  D  C  V  E  I  Y  G  P  P  T  N  P  E  A   312
AACTACAAGAACGTTGTGATATTTGGCAATCGCCAGGCGGATCGCTCTCCATGTGGGACAGGCACCAGCGCCAAGATGGCAACACTTTAT  1060
 N  Y  K  N  V  V  I  F  G  N  R  Q  A  D  R  S  P  C  G  T  G  T  S  A  K  M  A  T  L  Y   342
GCCAAAGGCCAGCTTCGCATCGGAGAGACTTTTGTGTACGAGAGCATACTCGGCTCACTCTTCCAGGGCAGGGTACTTGGGGAGGAGCGA  1150
 A  K  G  Q  L  R  I  G  E  T  F  V  Y  E  S  I  L  G  S  L  F  Q  G  R  V  L  G  E  E  R   372
ATACCGGGGGTGAAGGTGCCGGTGACCAAAGATGCCGAGGAAGGGATGCTCGTTGTAACGGCAGAAATTACTGGAAAGGCTTTTATCATG  1240
 I  P  G  V  K  V  P  V  T  K  D  A  E  E  G  M  L  V  V  T  A  E  I  T  G  K  A  F  I  M   402
GGTTTCAACACCATGCTGTTTGACCCAACGGATCCGTTTAAGAACGGATTCACATTAAAGCAGTAGATCTGGTAGAGCACAGAAACTATT  1330
 G  F  N  T  M  L  F  D  P  T  D  P  F  K  N  G  F  T  L  K  Q                              423
GGGGAACACGTGCGAACAGGTGCTGCTACGTGAAGGGTATTGAATGAATCGTTTTTTTTATTTTTATTTTTTATTTTTATTAGTGCATT  1420

ATTATTAAATTTTTTTTTTGTTTTGGGGTTTCAACGGTACCGCGTTGGGAGCAGGGAAGCGATAGCGGCCGGACAATTTTTTGCTTTTAT  1510

TTTCATTTTCATCTTCCTACCCAACCCCCTTGGTTCCACCGGTCGCGGCGGGGTCTTGTGGGTGGAGGAGTCCTAAATCCCGCACCTCGG  1600

AGGAATAAACATATTTCAATTTCATATCTTGGAATCAAAAGGCAT                                             1651
```

POLYADENILATION SITE

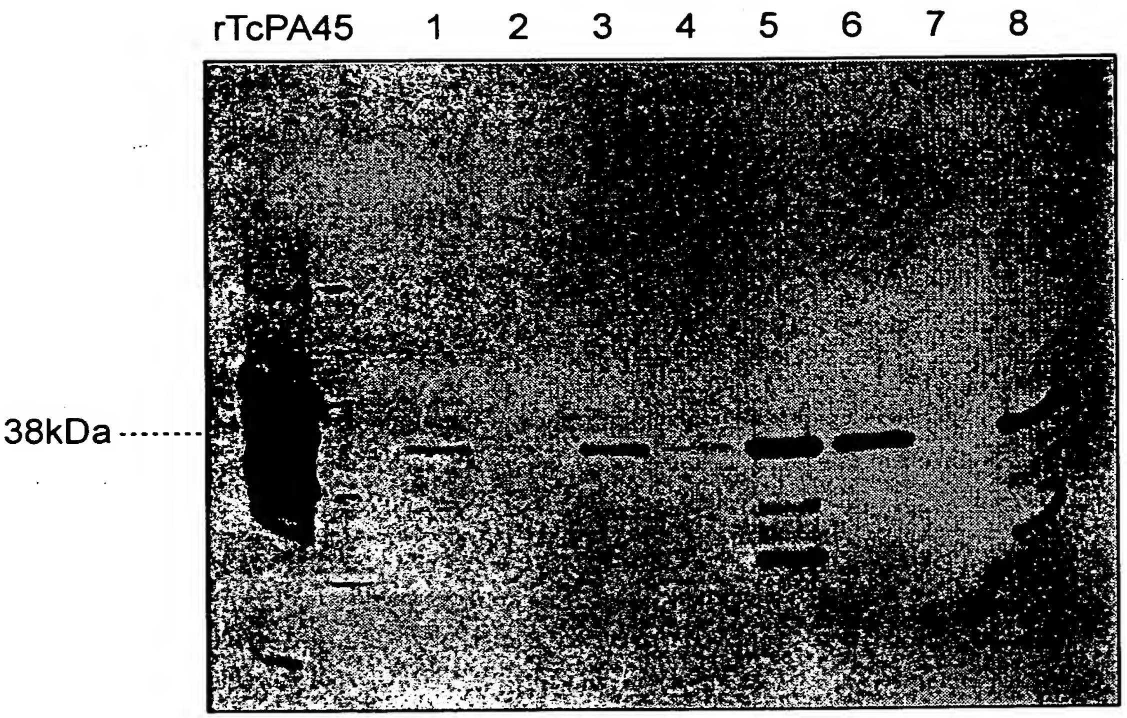
OBS: UNDERLINED THE SEQUENCED PEPTIDES USED TO DEDUCE DEGENERATED PRIMERS FOR CLONING

NUCLEOTIDE SEQUENCE AND PEPTIDE SEQUENCE TcPA45

FIG. 5B

Replacement Figure 6
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

WESTERN BLOT



LANE 3

SOLUBLE FRACTION OF EPIMASTIGOTES EXTRACT (CYTOSOLIC) REVEALED WITH ANTIBODY DIRECTED TO rTcPA45

----------- DEMONSTRATES THE EXISTANCE OF AN INTRACYTOPLASMIC FORM OF TcPA45 IN THE PARASITE

FIG. 6

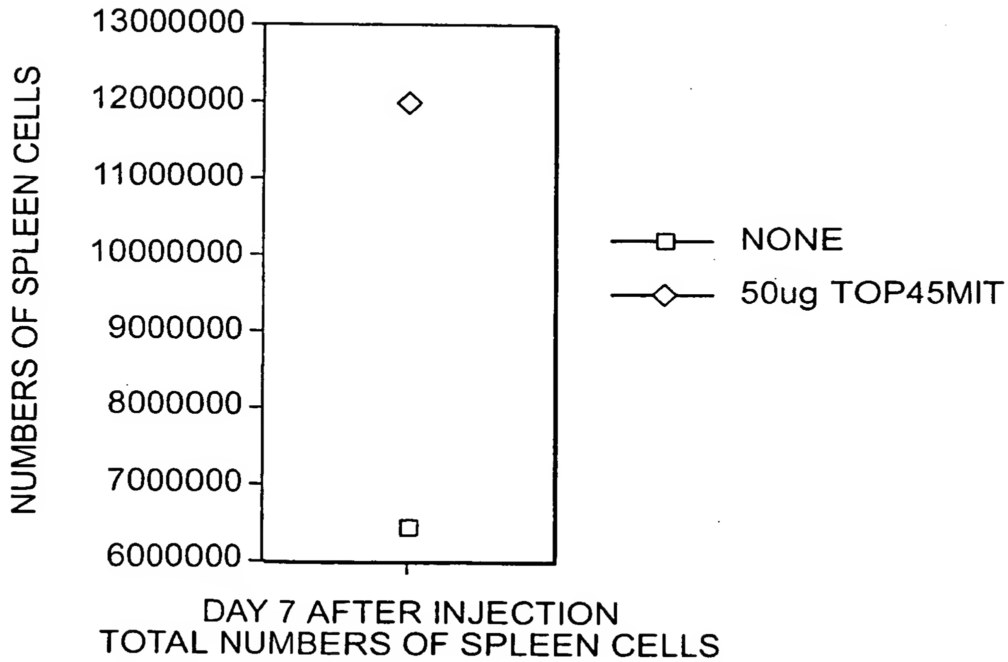

13000000
12000000
11000000
10000000
9000000
8000000
7000000
6000000
NUMBERS OF SPLEEN CELLS
NONE
50ug TOP45MIT
DAY 7 AFTER INJECTION
TOTAL NUMBERS OF SPLEEN CELLS

FIG. 7

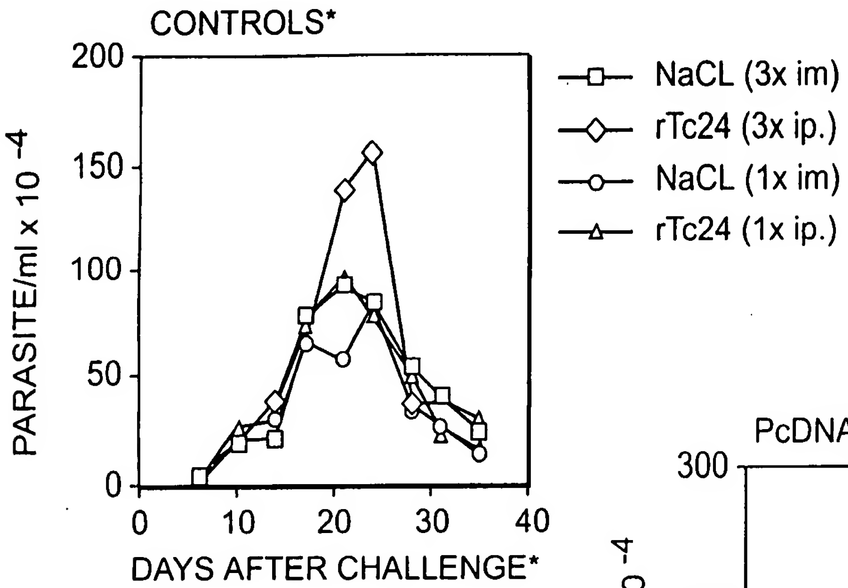

CONTROLS*
PARASITE/ml x 10 -4
200
150
100
50
0
0
10
20
30
40
DAYS AFTER CHALLENGE*
NaCL (3x im)
rTc24 (3x ip.)
NaCL (1x im)
rTc24 (1x ip.)

FIG. 8A

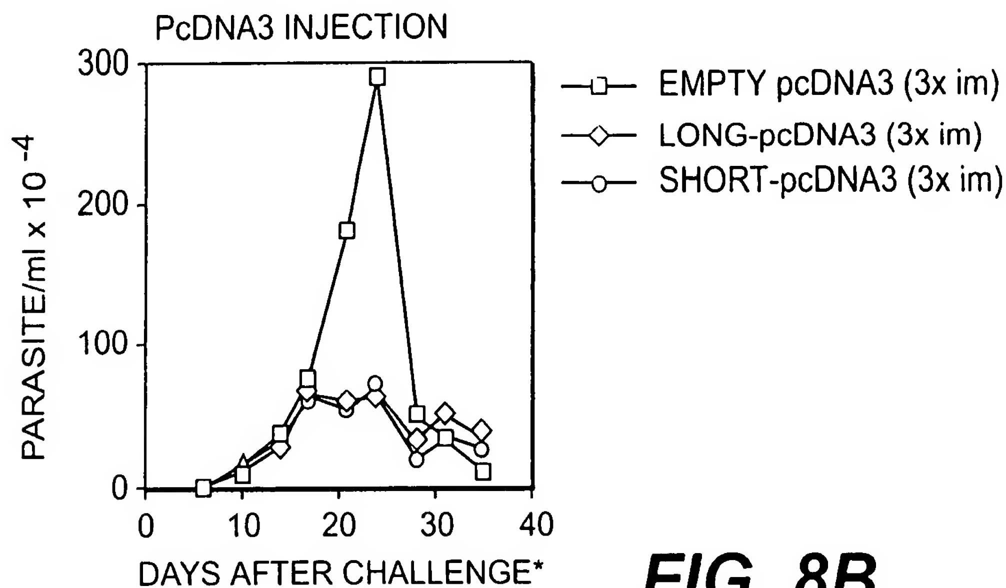

PcDNA3 INJECTION
PARASITE/ml x 10 -4
300
200
100
0
0
10
20
30
40
DAYS AFTER CHALLENGE*
EMPTY pcDNA3 (3x im)
LONG-pcDNA3 (3x im)
SHORT-pcDNA3 (3x im)

FIG. 8B

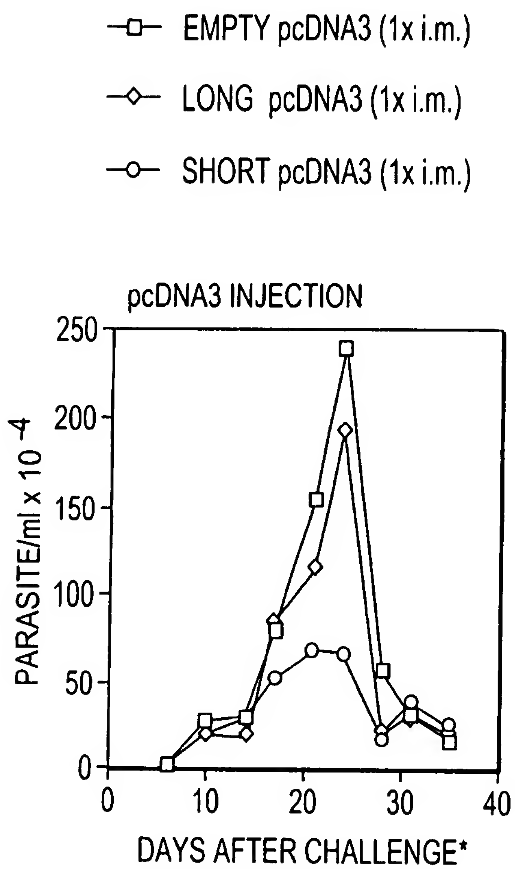


FIG. 8C

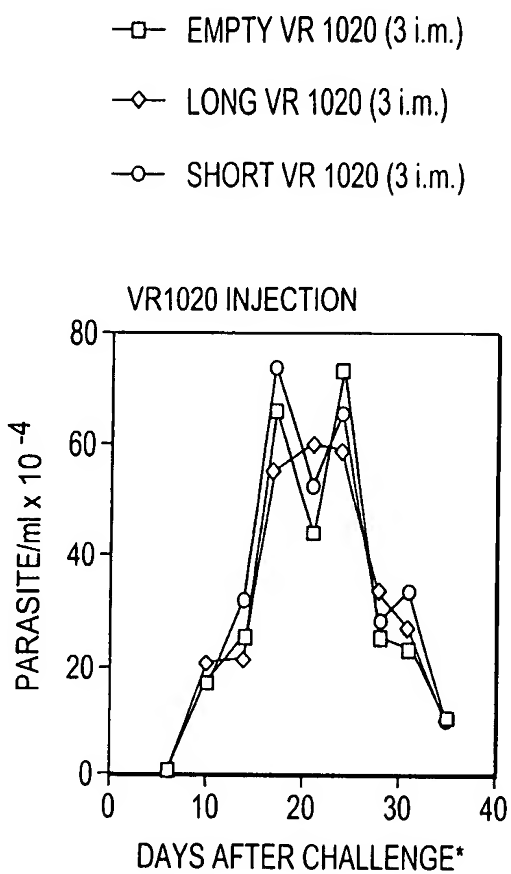


FIG. 8D

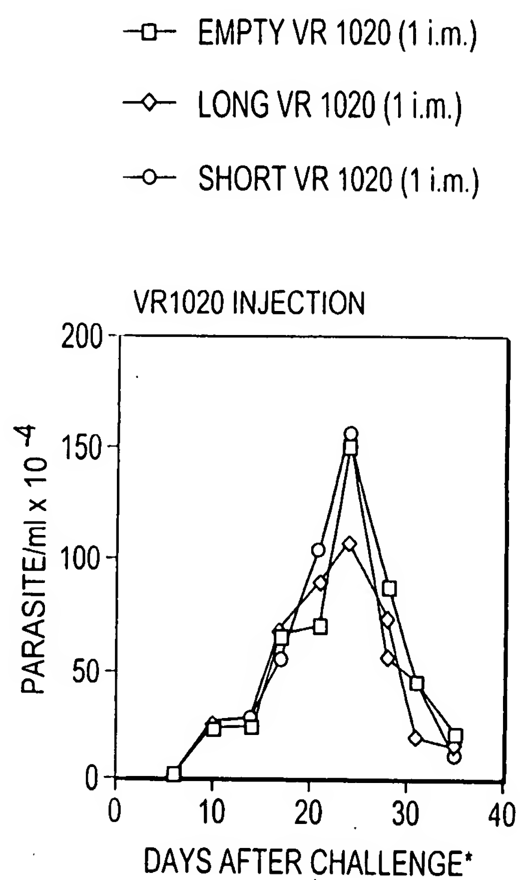


FIG. 8E

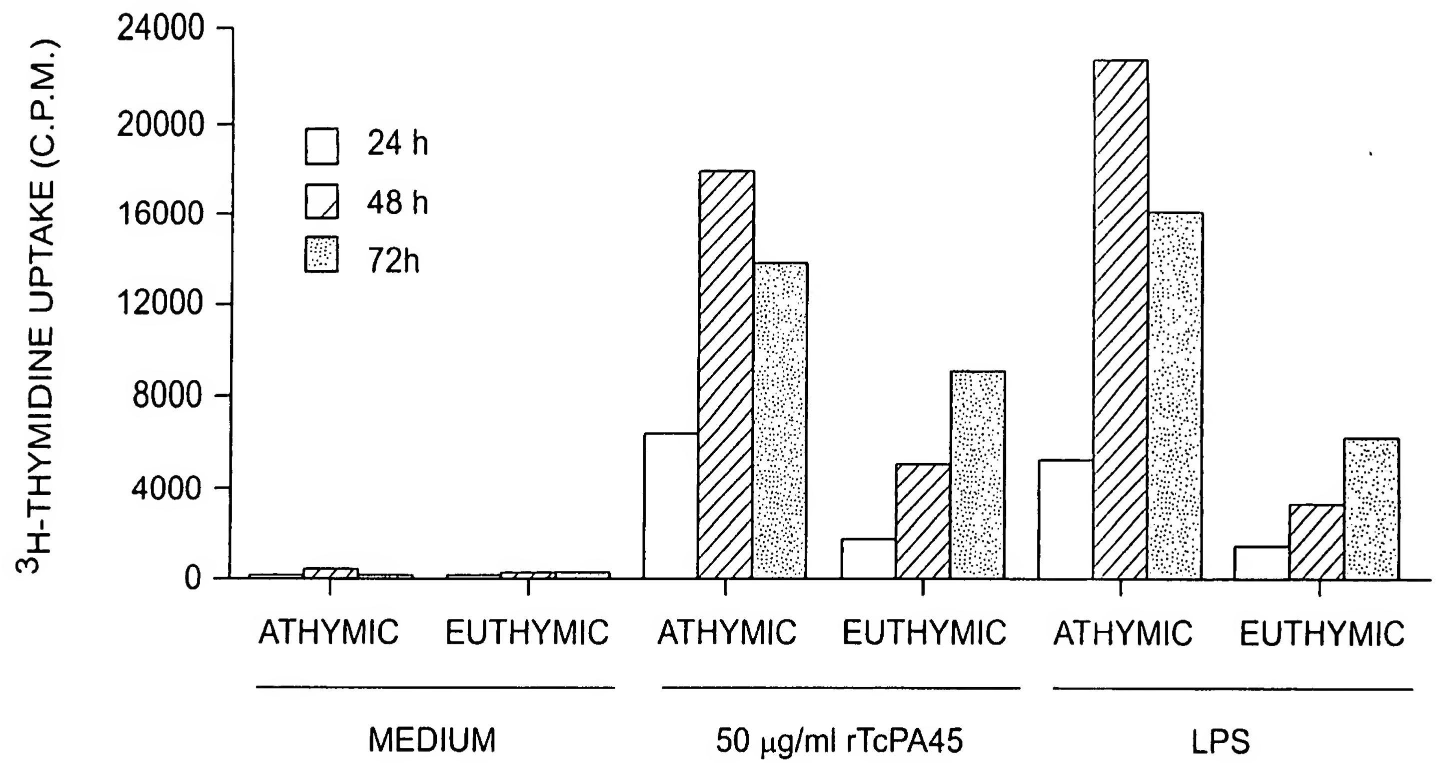

^{3}H-THYMIDINE UPTAKE (C.P.M.)
0
4000
8000
12000
16000
20000
24000
24 h
48 h
72h
ATHYMIC
EUTHYMIC
ATHYMIC
EUTHYMIC
ATHYMIC
EUTHYMIC
MEDIUM
50 µg/ml rTcPA45
LPS

FIG. 9

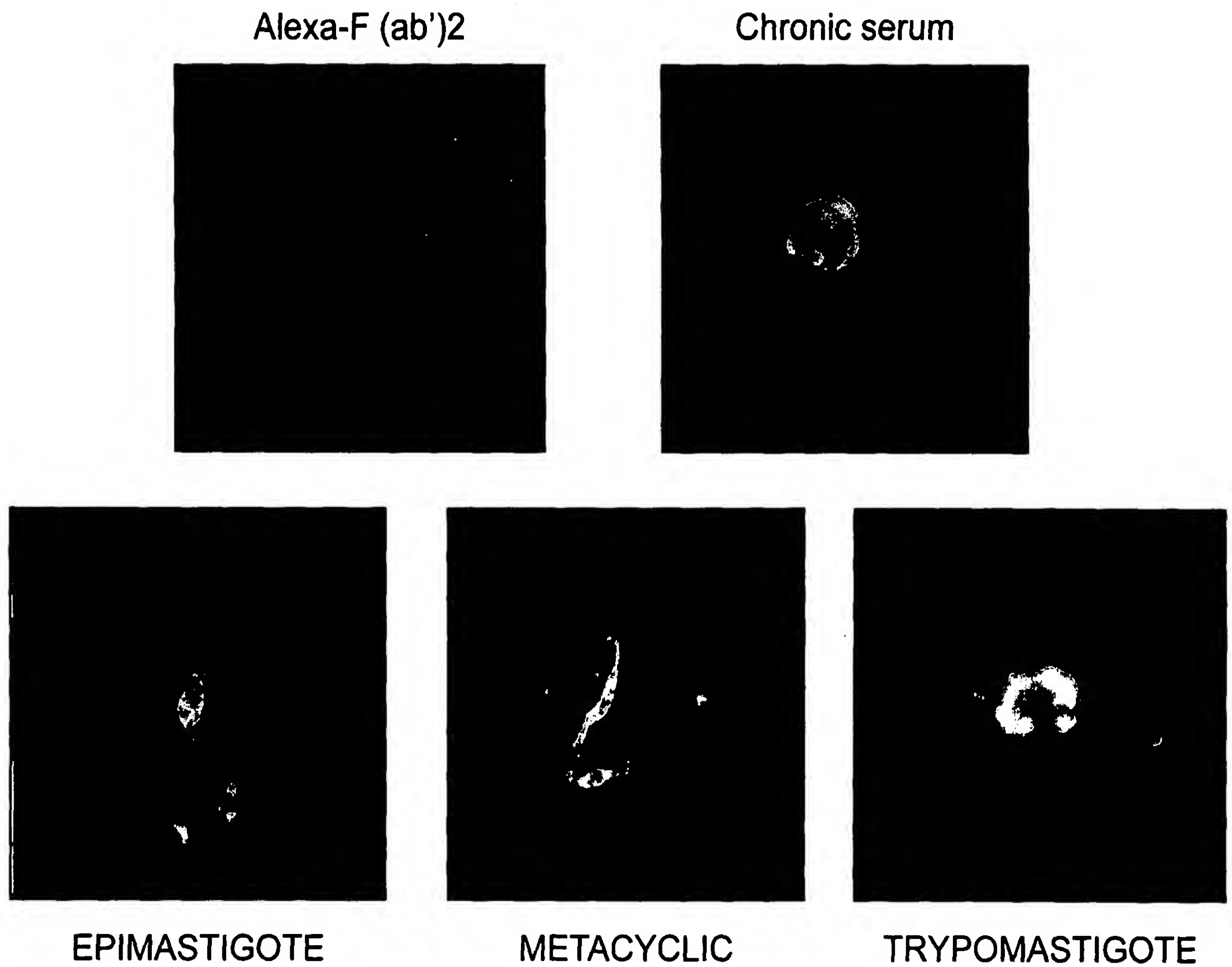

Alexa-F (ab')2
Chronic serum
EPIMASTIGOTE
METACYCLIC
TRYPOMASTIGOTE

FIG. 10A

Replacement Figure 10B
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

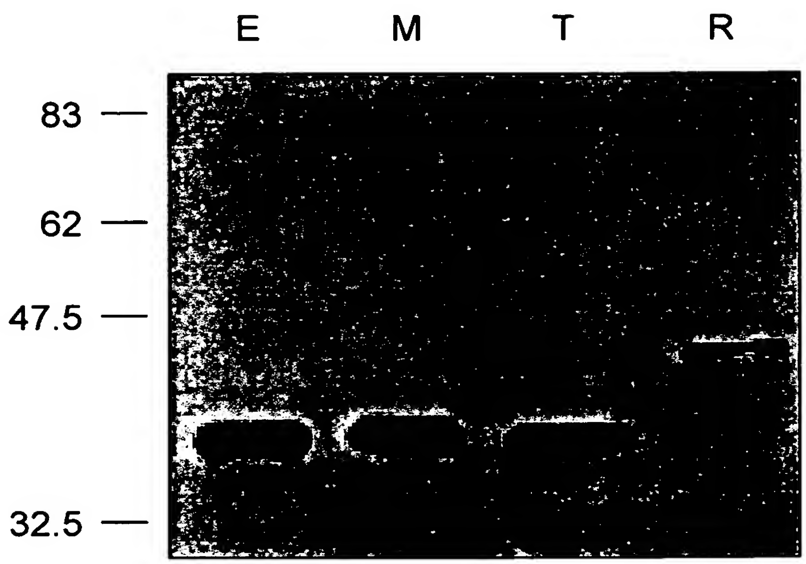


FIG. 10B

Replacement Figure 10C
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

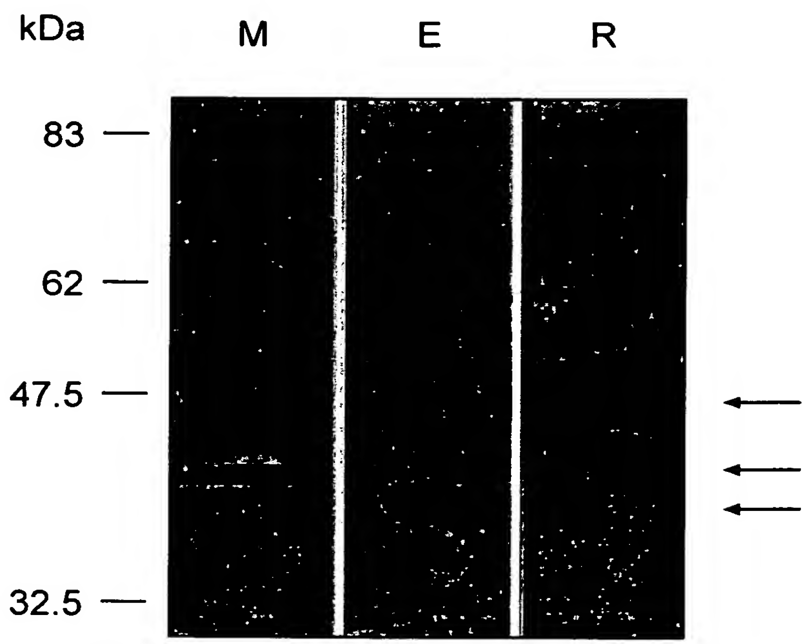


FIG. 10C

Replacement Figure 10D
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

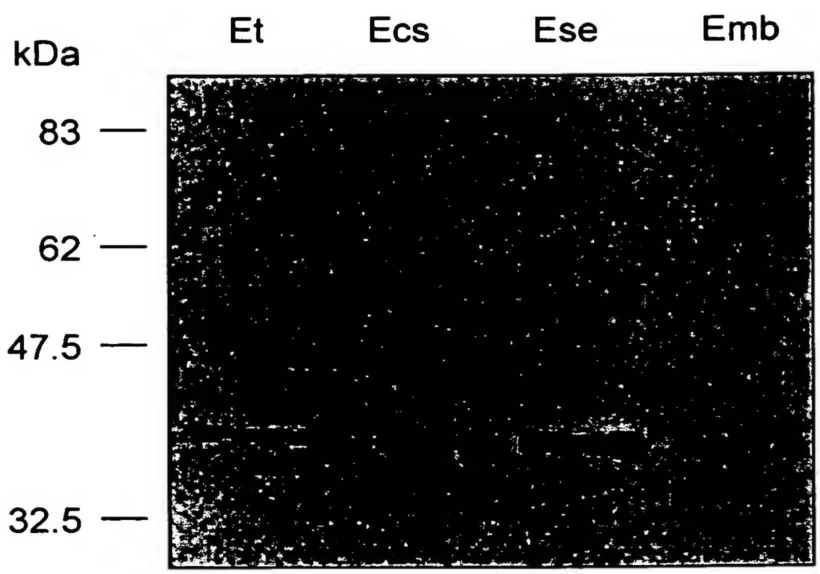


FIG. 10D

Replacement Figure 11A
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

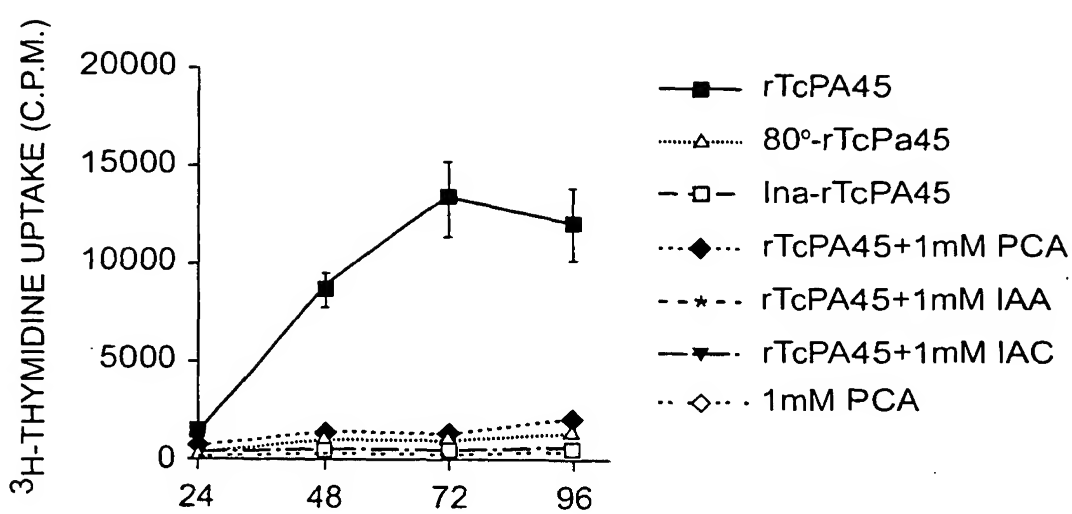


FIG. 11A

Replacement Figure 11B
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

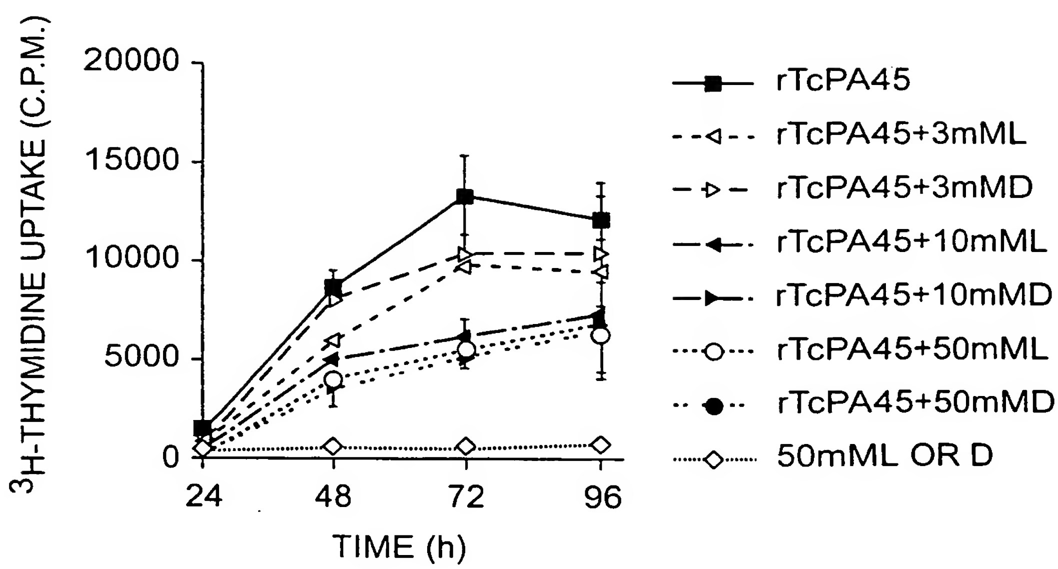


FIG. 11B

Replacement Figure 12
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

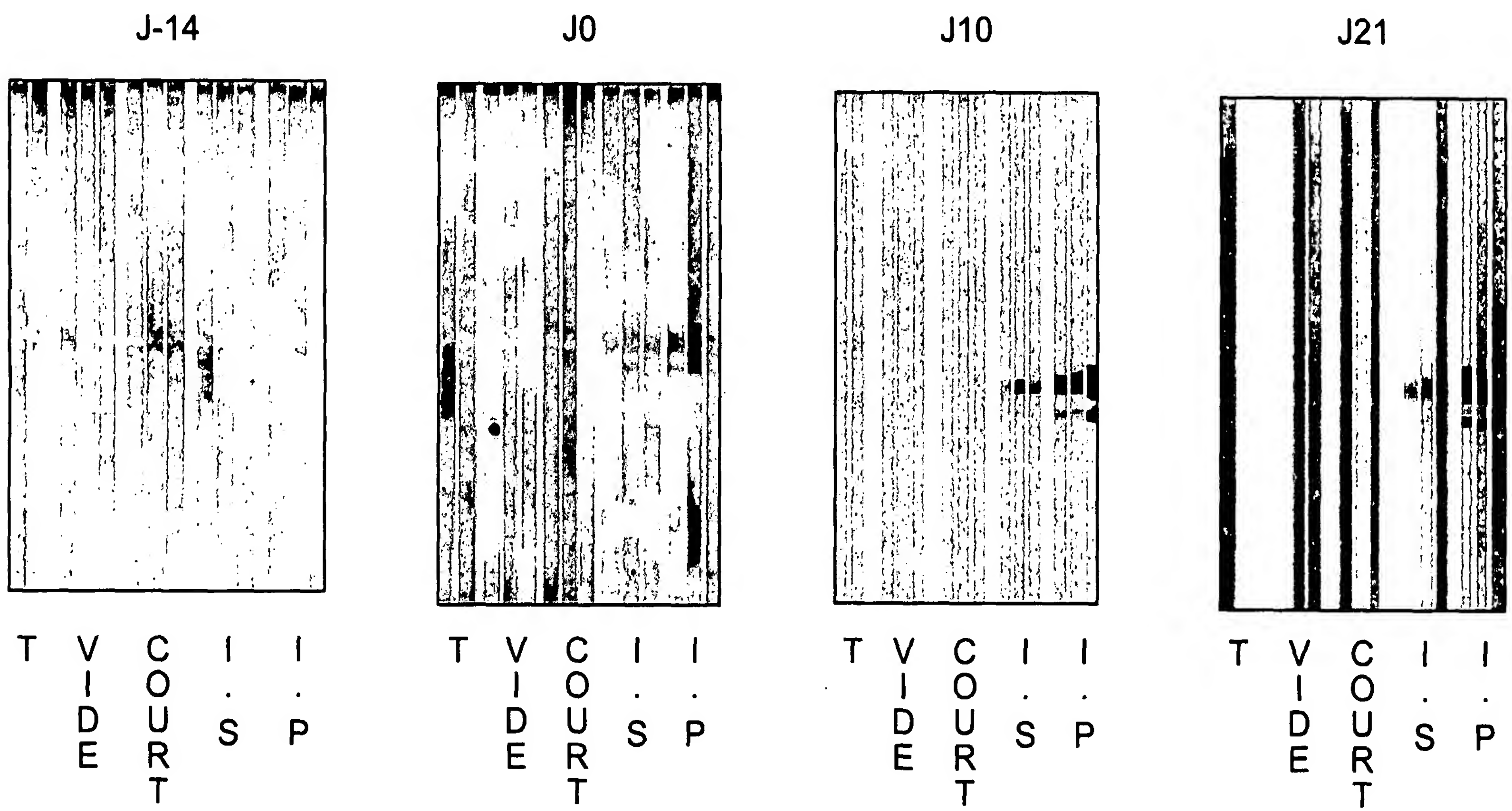


FIG. 12

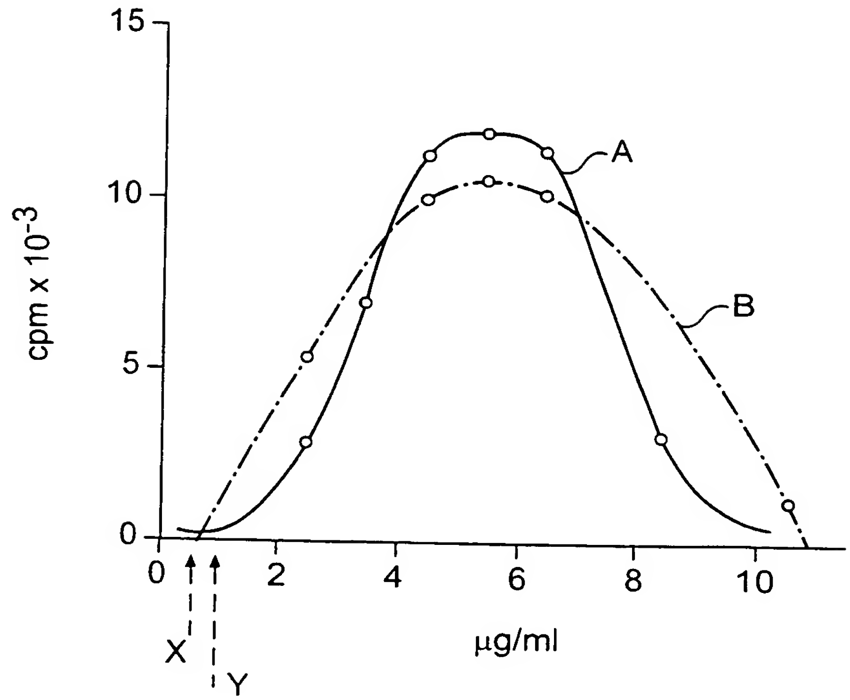


FIG. 13

Replacement Figure 14A and 14B
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

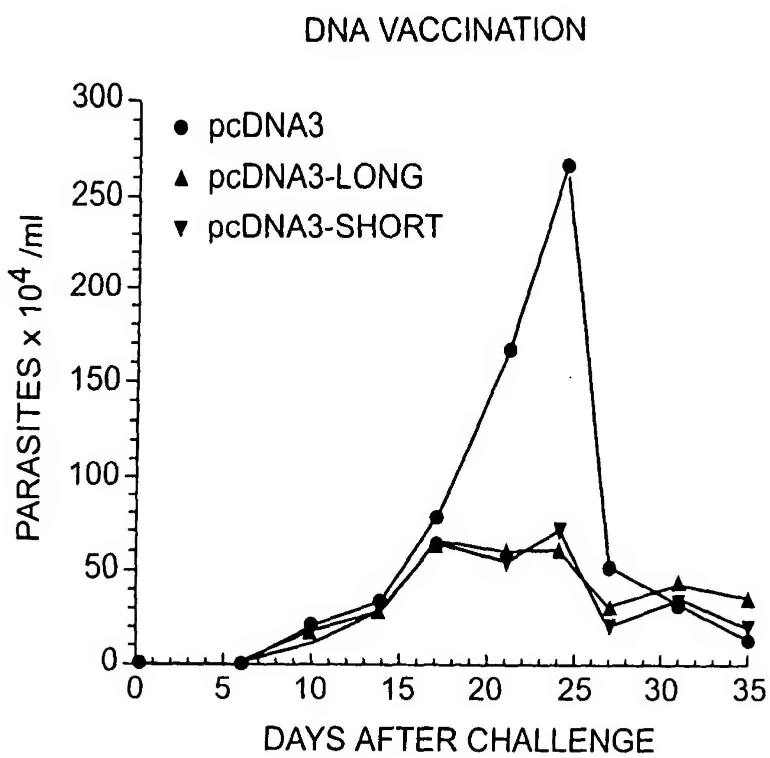


FIG. 14A

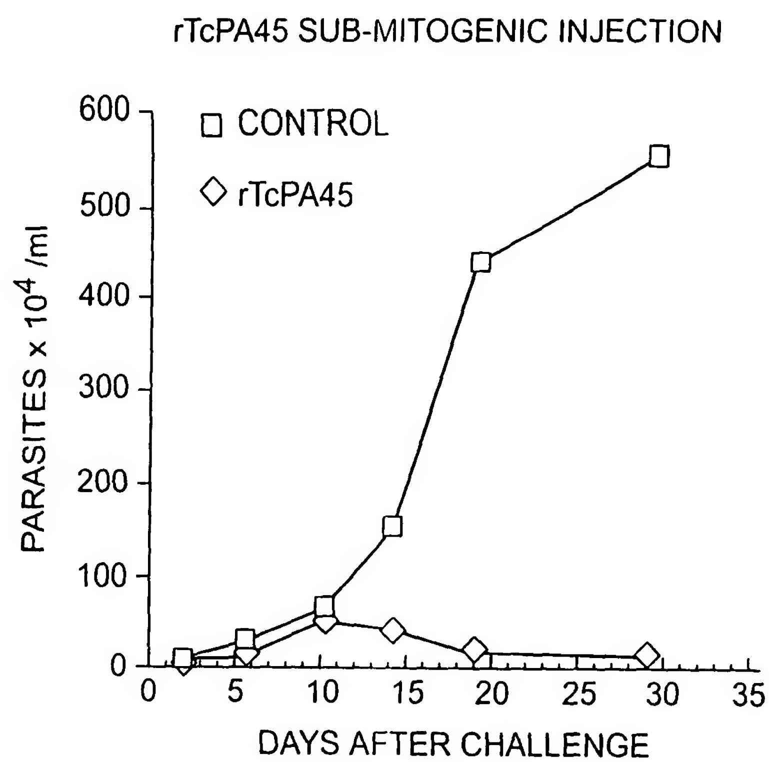


FIG. 14B

SEQ ID NO:2

Tc	RTGQEKLLFDQKYKIIKGEKKEKKKNQRANRREHQQKREIMRFKKS	75
Tc	FTCIDMHTEGEAARIVTSGLPHIPGSNMAEKKAYLQENMDYLRRGIMLEPRGHDDMFGAFLFDPIEEGADLGMVF	150
Tc	MDTGGYLNMCGHNSIAAVTAAVETGIVSVPAKATNVPVVLDTPAGLVRGTAHLQSGTESEVSNASIINVPSFLYQ	225
Tc	QDVVVVLPKPYGEVR*VDIAFGGNF*FAIVPAEQLGIDISVQNLSRLQEAGELLRTEINRSVKVQHPQLPHINTVDC	300
Tc	VEIYGPPTNPEANYK*NVVIFGNR*QADR SPCGT GTSAKMATLYAKGQLRIGETFVYESILGSLFQGRV--LGEE	371
Tc	RIPGVKVPVTKDAEEGMLVVTAEITGKAFIMGFNTMLFDPTDPFKNGFTLKQ*	423

FIG. 15

SEQ ID NO:4

Tc	MRFKKS	75
Tc	FTCIDMHTEGEAARIVTSGLPHIPGSNMAEKKAYLQENMDYLRRGIMLEPRGHDDMFGAFLFDPIEEGADLGMVF	150
Tc	MDTGGYLNMCGHNSIAAVTAAVETGIVSVPAKATNVPVVLDTPAGLVRGTAHLQSGTESEVSNASIINVPSFLYQ	225
Tc	QDVVVVLPKPYGEVR*VDIAFGGNF*FAIVPAEQLGIDISVQNLSRLQEAGELLRTEINRSVKVQHPQLPHINTVDC	300
Tc	VEIYGPPTNPEANYK*NVVIFGNR*QADR SPCGT GTSAKMATLYAKGQLRIGETFVYESILGSLFQGRV--LGEE	371
Tc	RIPGVKVPVTKDAEEGMLVVTAEITGKAFIMGFNTMLFDPTDPFKNGFTLKQ*	423

FIG. 16

SEQ ID NO:7

POLYPYRIMIDINE RICH REGION

SPLICE LEADER ACCEPTOR SITES

SIGNAL PEPTIDE

```
CCTTTTCTTTTTAAAAACAAAAAAAATTCCGGGGGGAATATGGAACAGGGTATATGCGTAAAAGTGTCTGTCCCAAACAAAAATTTTTT   90
                                                       M  R  K  S  V  C  P  K  Q  K  F  F   12
TTTTCCGCCTTCCCATTTTTTTTTTTTTTTTGTGTGTTTCCCTTGATCTCTCGAACAGGGCAGGAAAAGCTTCTGTTTGACCAAAAATAT  180
 F  S  A  F  P  F  F  F  F  F  C  V  F  P  L  I  S  R  T  G  Q  E  K  L  L  F  D  Q  K  Y   42
AAAATTATTAAGGGCGAGAAAAAAGAAAAGAAAAAAAAATCAACGAGCAAACAGGAGAGAACACCAACAAAAAAGGGAAATTATGCGATTT  270
 K  I  I  K  G  E  K  K  E  K  K  K  N  Q  R  A  N  R  R  E  K  Q  Q  K  R  E  I  M  R  F   72
AAGAAATCATTCACATGCATCGACATGCATACGGAAGGTGAAGCAGCACGGATTGTGACGAGTGGTTTGCCACACATTCCAGGTTCGAAT  360
 K  K  S  F  T  C  I  D  M  H  T  E  G  E  A  A  R  I  V  T  S  G  L  P  H  I  P  G  S  N  102
ATGGCGGAGAAGAAAGCATACCTGCAGGAAAACATGGATTATTTGAGGCGTGGCATAATGCTGGAACCACGTGGTCATGATGATATGTTT  430
 M  A  E  K  K  A  Y  L  Q  E  N  M  D  Y  L  R  R  G  I  M  L  E  P  R  G  K  D  D  M  F  132
GGAGCCTTTTTATTTGACCCTATTGAAGAAGGCGCTGACTTGGGCATGGTATTCATGGATACCGGTGGCTATTTAAATATGTGTGGACAT  520
 G  A  F  L  F  D  P  I  E  E  G  A  D  L  G  M  V  F  M  D  T  G  G  Y  L  N  M  C  G  H  162
AACTCAATTGCAGCGGTTACGGCGGCAGTTGAAACGGGAATTGTGAGCGTGCCGGCGAAGGCAACAAATGTTCCGGTTGTCCTGGACACA  610
 N  S  I  A  A  V  T  A  A  V  E  T  G  I  V  S  V  P  A  K  A  T  N  V  P  V  V  L  D  T  192
CCTGCGGGGTTGGTGCGCGGTACGGCACACCTTCAGAGTGGTACTGAGAGTGAGGTGTCAAATGCGAGTATTATCAATGTACCCTCATTT  700
 P  A  G  L  V  R  G  T  A  R  L  Q  S  G  T  E  S  E  V  S  N  A  S  I  I  N  V  P  S  F  222
TTGTATCAGCAGGATGTGGTGGTTGTGTTGCCAAAGCCCTATGGTGAAGTACGGGTTGATATTGCATTTGGAGGCAATTTTTTCGCCATT  790
 L  Y  Q  Q  D  V  V  V  V  L  P  K  P  Y  G  E  V  R  V  D  I  A  F  G  G  N  F  F  A  I  252
```

FIG. 17A

```
GTTCCCGCGGAGCAGTTGGGAATTGATATCTCCGTTCAAAACCTCTCCAGGCTGCAGGAGGCAGGAGAACTTCTGCGTACTGAAATCAAT  880
 V  P  A  E  Q  L  G  I  D  I  S  V  Q  N  L  S  R  L  Q  E  A  G  E  L  L  R  T  E  I  N   282
CGCAGTGTGAAGGTTCAGCACCCTCAGCTGCCCCATATTAACACTGTGGACTGTGTTGAGATATACGGTCCGCCAACGAACCCGGAGGCA  970
 R  S  V  K  V  Q  H  P  Q  L  P  H  I  N  T  V  D  C  V  E  I  Y  G  P  P  T  N  P  E  A   312
AACTACAAGAACGTTGTGATATTTGGCAATCGCCAGGCGGATCGCTCTCCATGTGGGACAGGCACCAGCGCCAAGATGGCAACACTTTAT 1060
 N  Y  K  N  V  V  I  F  G  N  R  Q  A  D  R  S  P  C  G  T  G  T  S  A  K  M  A  T  L  Y   342
GCCAAAGGCCAGCTTCGCATCGGAGAGACTTTTGTGTACGAGAGCATACTCGGCTCACTCTTCCAGGGCAGGGTACTTGGGGAGGAGCGA 1150
 A  K  G  Q  L  R  I  G  E  T  F  V  Y  E  S  I  L  G  S  L  F  Q  G  R  V  L  G  E  E  R   372
ATACCGGGGGTGAAGGTGCCGGTGACCAAAGATGCCGAGGAAGGGATGCTCGTTGTAACGGCAGAAATTACTGGAAAGGCTTTTATCATG 1240
 I  P  G  V  K  V  P  V  T  K  D  A  E  E  G  M  L  V  V  T  A  E  I  T  G  K  A  F  I  M   402
GGTTTCAACACCATGCTGTTTGACCCAACGGATCCGTTTAAGAACGGATTCACATTAAAGCAGTAGATCTGGTAGAGCACAGAAACTATT 1330
 G  F  N  T  M  L  F  D  P  T  D  P  F  K  N  G  F  T  L  K  Q  *                            423
GGGGAACACGTGCGAACAGGTGCTGCTACGTGAAGGGTATTGAATGAATCGTTTTTTTTATTTTTATTTTTTATTTTTATTAGTGCATT 1420

ATTATTAAATTTTTTTTTGTTTTGGGGTTTCAACGGTACCGCGTTGGGAGCAGGGAAGCGATAGCGGCCGGACAATTTTTTGCTTTTAT 1510

TTTCATTTTCATCTTCCTACCCAACCCCCTTGGTTCCACCGGTCGCGGCGGGGTCTTGTGGGTGGAGGAGTCCTAAATCCCGCACCTCGG 1600

AGGAATAAACATATTTCAATTTCATATCTTGGAATCAAAAGGCAT                                               1651
```

POLYADENILATION SITE

Obs: UNDERLINED THE SEQUENCED PEPTIDES USED TO DEDUCE DEGENERATED PRIMERS FOR CLONING

(b) NUCLEOTIDE SEQUENCE AND PEPTIDE SEQUENCE TcPA45

FIG. 17B

New Figure 18A
Divisional Application of 09/725,945
Inventors: Minoprio et al.
Attorney Docket No. 03495-0200-02000

SEQ ID NO:8

```
                                                                                     ATGCGTAAAAGTGTCTGTCCCAAACAAAAATTTTTT   90
                                                                                      M  R  K  S  V  C  P  K  Q  K  F  F   12
TTTTCCGCCTTCCCATTTTTTTTTTTTTTTGTGTGTTTCCCTTGATCTCTCGAACAGGGCAGGAAAAGCTTCTGTTTGACCAAAAATAT  180
 F  S  A  F  P  F  F  F  F  F  C  V  F  P  L  I  S  R  T  G  Q  E  K  L  L  F  D  Q  K  Y   42
AAAATTATTAAGGGCGAGAAAAAAGAAAAGAAAAAAAATCAACGAGCAAACAGGAGAGAACACCAACAAAAAAGGGAAATTATGCGATTT  270
 K  I  I  K  G  E  K  K  E  K  K  K  N  Q  R  A  N  R  R  E  H  Q  Q  K  R  E  I  M  R  F   72
AAGAAATCATTCACATGCATCGACATGCATACGGAAGGTGAAGCAGCACGGATTGTGACGAGTGGTTTGCCACACATTCCAGGTTCGAAT  360
 K  K  S  F  T  C  I  D  M  H  T  E  G  E  A  A  R  I  V  T  S  G  L  P  H  I  P  G  S  N  102
ATGGCGGAGAAGAAAGCATACCTGCAGGAAAACATGGATTATTTGAGGCGTGGCATAATGCTGGAACCACGTGGTCATGATGATATGTTT  430
 M  A  E  K  K  A  Y  L  Q  E  N  M  D  Y  L  R  R  G  I  M  L  E  P  R  G  H  D  D  M  F  132
GGAGCCTTTTTATTTGACCCTATTGAAGAAGGCGCTGACTTGGGCATGGTATTCATGGATACCGGTGGCTATTTAAATATGTGTGGACAT  520
 G  A  F  L  F  D  P  I  E  E  G  A  D  L  G  M  V  F  M  D  T  G  G  Y  L  N  M  C  G  H  162
AACTCAATTGCAGCGGTTACGGCGGCAGTTGAAACGGGAATTGTGAGCGTGCCGGCGAAGGCAACAAATGTTCCGGTTGTCCTGGACACA  610
 N  S  I  A  A  V  T  A  A  V  E  T  G  I  V  S  V  P  A  K  A  T  N  V  P  V  V  L  D  T  192
CCTGCGGGGTTGGTGCGCGGTACGGCACACCTTCAGAGTGGTACTGAGAGTGAGGTGTCAAATGCGAGTATTATCAATGTACCCTCATTT  700
 P  A  G  L  V  R  G  T  A  H  L  Q  S  G  T  E  S  E  V  S  N  A  S  I  I  N  V  P  S  F  222
TTGTATCAGCAGGATGTGGTGGTTGTGTTGCCAAAGCCCTATGGTGAAGTACGGGTTGATATTGCATTTGGAGGCAATTTTTTCGCCATT  790
 L  Y  Q  Q  D  V  V  V  V  L  P  K  P  Y  G  E  V  R  V  D  I  A  F  G  G  N  F  F  A  I  252
GTTCCCGCGGAGCAGTTGGGAATTGATATCTCCGTTCAAAACCTCTCCAGGCTGCAGGAGGCAGGAGAACTTCTGCGTACTGAAATCAAT  880
 V  P  A  E  Q  L  G  I  D  I  S  V  Q  N  L  S  R  L  Q  E  A  G  E  L  L  R  T  E  I  N  282
CGCAGTGTGAAGGTTCAGCACCCTCAGCTGCCCCATATTAACACTGTGGACTGTGTTGAGATATACGGTCCGCCAACGAACCCGGAGGCA  970
 R  S  V  K  V  Q  H  P  Q  L  P  H  I  N  T  V  D  C  V  E  I  Y  G  P  P  T  N  P  E  A  312
```

FIG. 18A

```
AACTACAAGAACGTTGTGATATTTGGCAATCGCCAGGCGGATCGCTCTCCATGTGGGACAGGCACCAGCGCCAAGATGGCAACACTTTAT 1060
 N  Y  K  N  V  V  I  F  G  N  R  Q  A  D  R  S  P  C  G  T  G  T  S  A  K  M  A  T  L  Y   342
GCCAAAGGCCAGCTTCGCATCGGAGAGACTTTTGTGTACGAGAGCATACTCGGCTCACTCTTCCAGGGCAGGGTACTTGGGGAGGAGCGA 1150
 A  K  G  Q  L  R  I  G  E  T  F  V  Y  E  S  I  L  G  S  L  F  Q  G  R  V  L  G  E  E  R   372
ATACCGGGGGTGAAGGTGCCGGTGACCAAAGATGCCGAGGAAGGGATGCTCGTTGTAACGGCAGAAATTACTGGAAAGGCTTTTATCATG 1240
 I  P  G  V  K  V  P  V  T  K  D  A  E  E  G  M  L  V  V  T  A  E  I  T  G  K  A  F  I  M   402
GGTTTCAACACCATGCTGTTTGACCCAACGGATCCGTTTAAGAACGGATTCACATTAAAGCAGTAGATCTGGTAGAGCACAGAAACTATT 1330
 G  F  N  T  M  L  F  D  P  T  D  P  F  K  N  G  F  T  L  K  Q  *                           423
GGGGAACACGTGCGAACAGGTGCTGCTACGTGAAGGGTATTGAATGAATCGTTTTTTTTATTTTATTTTTTATTTTATTAGTGCATT 1420

ATTATTAAATTTTTTTTTGTTTTGGGGTTTCAACGGTACCGCGTTGGGAGCAGGGAAGCGATAGCGGCCGGACAATTTTTTGCTTTTAT 1510

TTTCATTTTCATCTTCCTACCCAACCCCCTTGGTTCCACCGGTCGCGGCGGGGTCTTGTGGGTGGAGGAGTCCTAAATCCCGCACCTCGG 1600

AGGAATAAACATATTTCAATTTCATATCTTGGAATCAAAAGGCAT                                              1651
```

POLYADENILATION SITE

Obs: UNDERLINED THE SEQUENCED PEPTIDES USED TO DEDUCE DEGENERATED PRIMERS FOR CLONING

NUCLEOTIDE SEQUENCE AND PEPTIDE SEQUENCE TcPA45

FIG. 18B

SEQ ID NO:9

```
                                                                CGAACAGGGCAGGAAAAGCTTCTGTTTGACCAAAAATAT  270
                                                                 R  T  G  Q  E  K  L  L  F  D  Q  K  Y    72
AAAATTATTAAGGGCGAGAAAAAAGAAAAGAAAAAAAATCAACGAGCAAACAGGAGAGAACACCAACAAAAAAGGGAAATTATGCGATTT  360
 K  I  I  K  G  E  K  K  E  K  K  K  N  Q  R  A  N  R  R  E  H  Q  Q  K  R  E  I  M  R  F  102
AAGAAATCATTCACATGCATCGACATGCATACGGAAGGTGAAGCAGCACGGATTGTGACGAGTGGTTTGCCACACATTCCAGGTTCGAAT  430
 K  K  S  F  T  C  I  D  M  H  T  E  G  E  A  A  R  I  V  T  S  G  L  P  H  I  P  G  S  N  132
ATGGCGGAGAAGAAAGCATACCTGCAGGAAAACATGGATTATTTGAGGCGTGGCATAATGCTGGAACCACGTGGTCATGATGATATGTTT  520
 M  A  E  K  K  A  Y  L  Q  E  N  M  D  Y  L  R  R  G  I  M  L  E  P  R  G  H  D  D  M  F  162
GGAGCCTTTTTATTTGACCCTATTGAAGAAGGCGCTGACTTGGGCATGGTATTCATGGATACCGGTGGCTATTTAAATATGTGTGGACAT  610
 G  A  F  L  F  D  P  I  E  E  G  A  D  L  G  M  V  F  M  D  T  G  G  Y  L  N  M  C  G  H  192
AACTCAATTGCAGCGGTTACGGCGGCAGTTGAAACGGGAATTGTGAGCGTGCCGGCGAAGGCAACAAATGTTCCGGTTGTCCTGGACACA  700
 N  S  I  A  A  V  T  A  A  V  E  T  G  I  V  S  V  P  A  K  A  T  N  V  P  V  V  L  D  T  222
CCTGCGGGGTTGGTGCGCGGTACGGCACACCTTCAGAGTGGTACTGAGAGTGAGGTGTCAAATGCGAGTATTATCAATGTACCCTCATTT  790
 P  A  G  L  V  R  G  T  A  H  L  Q  S  G  T  E  S  E  V  S  N  A  S  I  I  N  V  P  S  F  252
TTGTATCAGCAGGATGTGGTGGTTGTGTTGCCAAAGCCCTATGGTGAAGTACGGGTTGATATTGCATTTGGAGGCAATTTTTTCGCCATT  880
 L  Y  Q  Q  D  V  V  V  V  L  P  K  P  Y  G  E  V  R  V  D  I  A  F  G  G  N  F  F  A  I  282
GTTCCCGCGGAGCAGTTGGGAATTGATATCTCCGTTCAAAACCTCTCCAGGCTGCAGGAGGCAGGAGAACTTCTGCGTACTGAAATCAAT  970
 V  P  A  E  Q  L  G  I  D  I  S  V  Q  N  L  S  R  L  Q  E  A  G  E  L  L  R  T  E  I  N  312
CGCAGTGTGAAGGTTCAGCACCCTCAGCTGCCCCATATTAACACTGTGGACTGTGTTGAGATATACGGTCCGCCAACGAACCCGGAGGCA 1060
 R  S  V  K  V  Q  H  P  Q  L  P  H  I  N  T  V  D  C  V  E  I  Y  G  P  P  T  N  P  E  A  342
AACTACAAGAACGTTGTGATATTTGGCAATCGCCAGGCGGATCGCTCTCCATGTGGGACAGGCACCAGCGCCAAGATGGCAACACTTTAT 1150
 N  Y  K  N  V  V  I  F  G  N  R  Q  A  D  R  S  P  C  G  T  G  T  S  A  K  M  A  T  L  Y  372
```

FIG. 19A

```
GCCAAAGGCCAGCTTCGCATCGGAGAGACTTTTGTGTACGAGAGCATACTCGGCTCACTCTTCCAGGGCAGGGTACTTGGGGAGGAGCGA 1240
 A  K  G  Q  L  R  I  G  E  T  F  V  Y  E  S  I  L  G  S  L  F  Q  G  R  V  L  G  E  E  R  402
ATACCGGGGGTGAAGGTGCCGGTGACCAAAGATGCCGAGGAAGGGATGCTCGTTGTAACGGCAGAAATTACTGGAAAGGCTTTTATCATG 1330
 I  P  G  V  K  V  P  V  T  K  D  A  E  E  G  M  L  V  V  T  A  E  I  T  G  K  A  F  I  M  423
GGTTTCAACACCATGCTGTTTGACCCAACGGATCCGTTTAAGAACGGATTCACATTAAAGCAGTAGATCTGGTAGAGCACAGAAACTATT 1420
 G  F  N  T  M  L  F  D  P  T  D  P  F  K  N  G  F  T  L  K  Q  *
GGGGAACACGTGCGAACAGGTGCTGCTACGTGAAGGGTATTGAATGAATCGTTTTTTTTTATTTTTATTTTTTATTTTTATTAGTGCATT 1510

ATTATTAAATTTTTTTTTTGTTTTGGGGTTTCAACGGTACCGCGTTGGGAGCAGGGAAGCGATAGCGGCCGGACAATTTTTTGCTTTTAT 1600

TTTCATTTTCATCTTCCTACCCAACCCCCTTGGTTCCACCGGTCGCGGCGGGGTCTTGTGGGTGGAGGAGTCCTAAATCCCGCACCTCGG 1651

AGGAATAAACATATTTCAATTTCATATCTTGGAATCAAAAGGCAT
```

POLYADENILATION SITE

Obs: UNDERLINED THE SEQUENCED PEPTIDES USED TO DEDUCE DEGENERATED PRIMERS FOR CLONING

NUCLEOTIDE SEQUENCE AND PEPTIDE SEQUENCE TcPA45

FIG. 19B

SEQ ID NO:10

<u>SIGNAL PEPTIDE</u>

<u>ATG</u>CGTAAAAGTGTCTGTCCCAAACAAAAATTTTTT

<u>TTTTCCGCCTTCCCATTTTTTTTTTTTTTTTGTGTGTTTCCCTTGATCTCT</u>

NUCLEOTIDE SEQUENCE OF SIGNAL SEQUENCE TcPA45

FIG. 20

SEQ ID NO:11

```
                                                                                ATGCGATTT  360
                                                                                 M  R  F   102
AAGAAATCATTCACATGCATCGACATGCATACGGAAGGTGAAGCAGCACGGATTGTGACGAGTGGTTTGCCACACATTCCAGGTTCGAAT  430
 K  K  S  F  T  C  I  D  M  H  T  E  G  E  A  A  R  I  V  T  S  G  L  P  H  I  P  G  S  N   132
ATGGCGGAGAAGAAAGCATACCTGCAGGAAAACATGGATTATTTGAGGCGTGGCATAATGCTGGAACCACGTGGTCATGATGATATGTTT  520
 M  A  E  K  K  A  Y  L  Q  E  N  M  D  Y  L  R  R  G  I  M  L  E  P  R  G  H  D  D  M  F   162
GGAGCCTTTTTATTTGACCCTATTGAAGAAGGCGCTGACTTGGGCATGGTATTCATGGATACCGGTGGCTATTTAAATATGTGTGGACAT  610
 G  A  F  L  F  D  P  I  E  E  G  A  D  L  G  M  V  F  M  D  T  G  G  Y  L  N  M  C  G  H   192
AACTCAATTGCAGCGGTTACGGCGGCAGTTGAAACGGGAATTGTGAGCGTGCCGGCGAAGGCAACAAATGTTCCGGTTGTCCTGGACACA  700
 N  S  I  A  A  V  T  A  A  V  E  T  G  I  V  S  V  P  A  K  A  T  N  V  P  V  V  L  D  T   222
CCTGCGGGGTTGGTGCGCGGTACGGCACACCTTCAGAGTGGTACTGAGAGTGAGGTGTCAAATGCGAGTATTATCAATGTACCCTCATTT  790
 P  A  G  L  V  R  G  T  A  H  L  Q  S  G  T  E  S  E  V  S  N  A  S  I  I  N  V  P  S  F   252
TTGTATCAGCAGGATGTGGTGGTTGTGTTGCCAAAGCCCTATGGTGAAGTACGGGTTGATATTGCATTTGGAGGCAATTTTTTCGCCATT  880
 L  Y  Q  Q  D  V  V  V  V  L  P  K  P  Y  G  E  V  R  V  D  I  A  F  G  G  N  F  F  A  I   282
GTTCCCGCGGAGCAGTTGGGAATTGATATCTCCGTTCAAAACCTCTCCAGGCTGCAGGAGGCAGGAGAACTTCTGCGTACTGAAATCAAT  970
 V  P  A  E  Q  L  G  I  D  I  S  V  Q  N  L  S  R  L  Q  E  A  G  E  L  L  R  T  E  I  N   312
CGCAGTGTGAAGGTTCAGCACCCTCAGCTGCCCCATATTAACACTGTGGACTGTGTTGAGATATACGGTCCGCCAACGAACCCGGAGGCA 1060
 R  S  V  K  V  Q  H  P  Q  L  P  H  I  N  T  V  D  C  V  E  I  Y  G  P  P  T  N  P  E  A   342
AACTACAAGAACGTTGTGATATTTGGCAATCGCCAGGCGGATCGCTCTCCATGTGGGACAGGCACCAGCGCCAAGATGGCAACACTTTAT 1150
 N  Y  K  N  V  V  I  F  G  N  R  Q  A  D  R  S  P  C  G  T  G  T  S  A  K  M  A  T  L  Y   372
GCCAAAGGCCAGCTTCGCATCGGAGAGACTTTTGTGTACGAGAGCATACTCGGCTCACTCTTCCAGGGCAGGGTACTTGGGGAGGAGCGA 1240
 A  K  G  Q  L  R  I  G  E  T  F  V  Y  E  S  I  L  G  S  L  F  Q  G  R  V  L  G  E  E  R   402
```

FIG. 21A

```
ATACCGGGGGTGAAGGTGCCGGTGACCAAAGATGCCGAGGAAGGGATGCTCGTTGTAACGGCAGAAATTACTGGAAAGGCTTTTATCATG 1330
 I  P  G  V  K  V  P  V  T  K  D  A  E  E  G  M  L  V  V  T  A  E  I  T  G  K  A  F  I  M   423
GGTTTCAACACCATGCTGTTTGACCCAACGGATCCGTTTAAGAACGGATTCACATTAAAGCAGTAGATCTGGTAGAGCACAGAAACTATT 1420
 G  F  N  T  M  L  F  D  P  T  D  P  F  K  N  G  F  T  L  K  Q  *
GGGGAACACGTGCGAACAGGTGCTGCTACGTGAAGGGTATTGAATGAATCGTTTTTTTTTATTTTTATTTTTTATTTTTATTAGTGCATT 1510

ATTATTAAATTTTTTTTTTGTTTTGGGGTTTCAACGGTACCGCGTTGGGAGCAGGGAAGCGATAGCGGCCGGACAATTTTTTGCTTTTAT 1600

TTTCATTTTCATCTTCCTACCCAACCCCCTTGGTTCCACCGGTCGCGGCGGGGTCTTGTGGGTGGAGGAGTCCTAAATCCCGCACCTCGG 1651

AGGAATAAACATATTTCAATTTCATATCTTGGAATCAAAAGGCAT
```

FIG. 21B